SEQUENCE LISTING

<110> Lohning, Corinna

<120> Novel methods for displaying (poly)peptides/proteins on bacteriophage particles via disulfide bonds

<130> MORPHO/11

<140> PCT/EP00/06968

<141> 2000-07-20

<150> EP 99114072.4

<151> 1999-07-20

<150> EP 00103551.8

<151> 2000-02-18

<160> 41

<170> PatentIn version 3.0

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Ile Glu Gly Arg His His His His His His
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<213> artificial sequence

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Asp Tyr Cys Asp Ile Glu Phe
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<220>
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Glu Phe Ser His His His His His His
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<220>
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<400> 6

Ser Ala Trp Ser His Pro Gln Phe Glu Lys
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<210> 7

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<223> Description of Artificial Sequence: synthetic module

<400> 7

Thr Met Ala Cys Asp Ile Glu Phe
1 5

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<220>
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Asp Tyr Lys Asp Asp Asp Asp Lys
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<400> 9

Trp Ser His Pro Gln Phe Glu Lys
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Pro Gly Gly Ser Gly
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Cys His His His His His His
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His His His His His His Cys
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His

<210> 15

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Arg Ser Gly Ala Tyr Asp Tyr
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Gln Gln Tyr Ser Ser Phe Pro Leu
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His Gln Val Tyr Ser Thr Ser Pro
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Phe Pro Tyr Thr Tyr His Gly Phe Met Asp Asn
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<400> 22

Gln Ser Tyr Asp Ser Gly Asn Leu
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<210> 23

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Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe Thr Asn Val
35 40 45

Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys
50 55 60

Leu Trp Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln
65 70 75 80

Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu
85 90 95

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
100 105 110

Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr
115 120 125

Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln
130 135 140

Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn
145 150 155 160

Thr Phe Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu
165 170 175

Thr Val Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr
180 185 190

Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr
195 200 205

Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu
210 215 220

Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln
225 230 235 240

Pro Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
245 250 255

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
260 265 270

Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr
275 280 285

Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp
290 295 300

Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala
305 310 315 320

Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly
325 330 335

Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser
340 345 350

Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn
355 360 365

Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro
370 375 380

Tyr Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp
385 390 395 400

Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala
405 410 415

Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys
420 425 430

Glu Ser

<210> 24

<211> 219

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<400> 24

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
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Thr Val Ala Gln Ala Asp Tyr Cys Asp Ile Glu Phe Asn Ala Gly Gly
20 25 30

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
35 40 45

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly
50 55 60

Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn
65 70 75 80

Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp
85 90 95

Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile
100 105 110

Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala
115 120 125

Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp
130 135 140

Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser
145 150 155 160

Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys
165 170 175

Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly
180 185 190

Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser
195 200 205

Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
210 215

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<211> 432

<212> PRT

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<400> 25

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
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His Ser Thr Met Ala Cys Asp Ile Glu Phe Ala Glu Thr Val Glu Ser
20 25 30

Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys
35 40 45

Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp
50 55 60

Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr
65 70 75 80

Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu Gly Gly
85 90 95

Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
100 105 110

Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr
115 120 125

Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro
130 135 140

Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe
145 150 155 160

Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val
165 170 175

Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr
180 185 190

Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn
195 200 205

Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro
210 215 220

Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro
225 230 235 240

Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu
245 250 255

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
260 265 270

Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys
275 280 285

Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn
290 295 300

Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp
305 310 315 320

Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala
325 330 335

Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met
340 345 350

Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg
355 360 365

Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Tyr Val
370 375 380

Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile
385 390 395 400

Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe
405 410 415

Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
420 425 430

<210> 26

<211> 434

<212> PRT

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic module

<400> 26

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

Thr Val Ala Gln Ala Asp Tyr Cys Asp Ile Glu Phe Ala Glu Thr Val
20 25 30

Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe Thr Asn Val
35 40 45

Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys
50 55 60

Leu Trp Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln
65 70 75 80

Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu
85 90 95

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
100 105 110

Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr
115 120 125

Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln
130 135 140

Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn
145 150 155 160

Thr Phe Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu
165 170 175

Thr Val Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr
180 185 190

Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr
195 200 205

Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu
210 215 220

Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln
225 230 235 240

Pro Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
245 250 255

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
260 265 270

Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr
275 280 285

Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp
290 295 300

Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala
305 310 315 320

Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly
325 330 335

Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser
340 345 350

Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn
355 360 365

Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro
370 375 380

Tyr Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp
385 390 395 400

Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala
405 410 415

Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys
420 425 430

Glu Ser

<210> 27

<211> 219

<212> PRT

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic module

<400> 27

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Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
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Thr Val Ala Gln Ala Asp Tyr Cys Asp Ile Glu Phe Asn Ala Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
        35                  40                  45

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly
    50                  55                  60

Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn
65                  70                  75                  80

Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp
                85                  90                  95

Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile
            100                 105                 110

Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala
        115                 120                 125

Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp
    130                 135                 140

Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser
145                 150                 155                 160

Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys
                165                 170                 175

Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly
            180                 185                 190

Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser
        195                 200                 205

Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
    210                 215
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Thr Val Ala Gln Ala Asp Tyr Cys Asp Ile Glu Phe Gly Gly Gly Gly
20 25 30

Ser Met Ser Val Leu Val Tyr Ser Phe Ala Ser Phe Val Leu Gly Trp
35 40 45

Cys Leu Arg Ser Gly Ile Thr Tyr Phe Thr Arg Leu Met Glu Thr Ser
50 55 60

Ser
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<210> 29

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<400> 29

Ser Pro Gly Gly Ser Gly Gly Ala Pro His His His His His His Cys
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1 5 10 15

Pro Gln Phe Glu Lys
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<210> 31

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<400> 31

Glu Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Pro
1 5 10 15

Trp Ser His Pro Gln Phe Glu Lys
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<210> 32

<211> 17

<212> PRT

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic module

<400> 32

Glu Phe Pro Gly Gly Ser Gly Gly Ala Pro His His His His His His
1 5 10 15

Cys

<210> 33

<211> 22

<212> PRT

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<220>
<223> Description of Artificial Sequence: synthetic module

<400> 33

Cys Glu Phe Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Pro Trp Ser
1 5 10 15

His Pro Gln Phe Glu Lys
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<210> 34

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<212> PRT

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: synthetic module

<400> 34

Cys Glu Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
1 5 10 15

Pro Trp Ser His Pro Gln Phe Glu Lys
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cggtagtgat cttatttcat tatggtgaaa gttggaacct cacccgacgt ctaatgtgag 4260

ttagctcact cattaggcac cccaggcttt acactttatg cttccggctc gtatgttgtg 4320

tggaattgtg agcggataac aatttcacac aggaaacagc tatgaccatg attacgaatt 4380

<210> 36

<211> 2839

<212> DNA

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: vector

<400> 36
acccgacacc atcgaaatta atacgactca ctatagggag accacaacgg tttcccgaat 60

tgtgagcgga taacaataga ataatttttg tttaacttta agaaggagat atatccatgg 120

ctgaaactgt tgaaagttgt ttagcaaaat cccatacaga aaattcattt actaacgtct 180

ggaaagacga caaaacttta gatcgttacg ctaactatga gggctgtctg tggaatgcta 240

caggcgttgt agtttgtact ggtgacgaaa ctcagtgtta cggtacatgg gttcctattg 300

ggcttgctat ccctgaaaat gagggtggtg gctctgaggg tggcggttct ccgtacgacg 360

ttccagacta cgcttccctg cgttcccatc accatcacca tcactaagct tcagtcccgg 420

gcagtggatc cggctgctaa caaagcccga aaggaagctg agttggctgc tgccaccgct 480

gagcaataac tagcataacc ccttggggcc tctaaacggg tcttgagggg ttttttgctg 540

aaaggaggaa ctatatccgg atcgagatcc ccacgcgccc tgtagcggcg cattaagcgc 600

ggcgggtgtg gtggttacgc gcagcgtgac cgctacactt gccagcgccc tagcgcccgc 660

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aaatcggggc atcccttag ggttccgatt tagtgcttta cggcacctcg accccaaaaa 780

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caaccctatc tcggtctatt cttttgattt ataagggatt ttgccgattt cggcctattg 960

gttaaaaaat gagctgattt aacaaaaatt taacgcgaat tttaacaaaa tattaacgtt 1020

tacaatttca ggtggcactt ttcggggaaa tgtgcgcgga acccctattt gtttatttt 1080

ctaaatacat tcaaatatgt atccgctcat gagacaataa ccctgataaa tgcttcaata 1140

atattgaaaa aggaagagta tgagtattca acatttccgt gtcgcccttа ttccctttt 1200

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tgaagatcag ttgggtgcac gagtgggtta catcgaactg gatctcaaca gcggtaagat 1320

ccttgagagt tttcgccccg aagaacgttt tccaatgatg agcactttta aagttctgct 1380

atgtggcgcg gtattatccc gtattgacgc cgggcaagag caactcggtc gccgcataca 1440

ctattctcag aatgacttgg ttgagtactc accagtcaca gaaaagcatc ttacggatgg 1500

catgacagta agagaattat gcagtgctgc cataaccatg agtgataaca ctgcggccaa 1560

cttacttctg acaacgatcg gaggaccgaa ggagctaacc gcttttttgc acaacatggg 1620

ggatcatgta actcgccttg atcgttggga accggagctg aatgaagcca taccaaacga 1680

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ccgtatcgta gttatctaca cgacggggag tcaggcaact atggatgaac gaaatagaca 1980

gatcgctgag ataggtgcct cactgattaa gcattggtaa ctgtcagacc aagtttactc 2040

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ccttttttgat aatctcatga ccaaaatccc ttaacgtgag ttttcgttcc actgagcgtc 2160

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ctgcttgcaa acaaaaaaac caccgctacc agcggtggtt tgtttgccgg atcaagagct 2280

accaactctt tttccgaagg taactggctt cagcagagcg cagataccaa atactgtcct 2340

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cagggtcgga acaggagagc gcacgaggga gcttccaggg ggaaacgcct ggtatcttta 2700

tagtcctgtc gggtttcgcc acctctgact tgagcgtcga tttttgtgat gctcgtcagg 2760

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ctggcctttt gctcacatg 2839

<210> 37

<211> 4045

<212> DNA

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: vector

<400> 37
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tctggatttg ttcagaacgc tcggttgccg ccgggcgttt tttattggtg agaatccaag 120

ctagcttggc gagattttca ggagctaagg aagctaaaat ggagaaaaaa atcactggat 180

ataccaccgt tgatatatcc caatggcatc gtaaagaaca ttttgaggca tttcagtcag 240

ttgctcaatg tacctataac cagaccgttc agctggatat tacggccttt ttaaagaccg 300

taaagaaaaa taagcacaag ttttatccgg cctttattca cattcttgcc cgcctgatga 360

atgctcatcc ggaatttcgt atggcaatga aagacggtga gctggtgata tgggatagtg 420

ttcacccttg ttacaccgtt ttccatgagc aaactgaaac gttttcatcg ctctggagtg 480

aataccacga cgatttccgg cagtttctac acatatattc gcaagatgtg gcgtgttacg 540

gtgaaaacct ggcctatttc cctaaagggt ttattgagaa tatgtttttc gtctcagcca 600

atccctgggt gagtttcacc agttttgatt taaacgtggc caatatggac aacttcttcg 660

cccccgtttt caccatgcat gggcaaatat tatacgcaag gcgacaaggt gctgatgccg 720

ctggcgattc aggttcatca tgccgtctgt gatggcttcc atgtcggcag aatgcttaat 780

gaattacaac agtactgcga tgagtggcag ggcggggcgt aatttttttа aggcagttat 840

tggtgccctt aaacgcctgg ggtaatgact ctctagcttg aggcatcaaa taaaacgaaa 900

ggctcagtcg aaagactggg cctttcgttt tatctgttgt ttgtcggtga acgctctcct 960

gagtaggaca aatccgccgc tctagagctg cctcgcgcgt ttcggtgatg acggtgaaaa 1020

cctctgacac atgcagctcc cggagacggt cacagcttgt ctgtaagcgg atgccgggag 1080

cagacaagcc cgtcagggcg cgtcagcggg tgttggcggg tgtcggggcg cagccatgac 1140

ccagtcacgt agcgatagcg gagtgtatac tggcttaact atgcggcatc agagcagatt 1200

gtactgagag tgcaccatat gcggtgtgaa ataccgcaca gatgcgtaag gagaaaatac 1260

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cggcgagcgg tatcagctca ctcaaaggcg gtaatacggt tatccacaga atcaggggat 1380

aacgcaggaa agaacatgtg agcaaaaggc cagcaaaagg ccaggaaccg taaaaaggcc 1440

gcgttgctgg cgtttttcca taggctccgc ccccctgacg agcatcacaa aaatcgacgc 1500

tcaagtcaga ggtggcgaaa cccgacagga ctataaagat accaggcgtt tccccctgga 1560

agctccctcg tgcgctctcc tgttccgacc ctgccgctta ccggatacct gtccgccttt 1620

ctcccttcgg gaagcgtggc gctttctcaa tgctcacgct gtaggtatct cagttcggtg 1680

taggtcgttc gctccaagct gggctgtgtg cacgaacccc ccgttcagcc cgaccgctgc 1740

gccttatccg gtaactatcg tcttgagtcc aacccggtaa gacacgactt atcgccactg 1800

gcagcagcca ctggtaacag gattagcaga gcgaggtatg taggcggtgc tacagagttc 1860

ttgaagtggt ggcctaacta cggctacact agaaggacag tatttggtat ctgcgctctg 1920

ctgaagccag ttaccttcgg aaaaagagtt ggtagctctt gatccggcaa acaaaccacc 1980

gctggtagcg gtggtttttt tgtttgcaag cagcagatta cgcgcagaaa aaaaggatct 2040

caagaagatc ctttgatctt ttctacgggg tctgacgctc agtggaacga aaactcacgt 2100

taagggattt tggtcatgag attatcaaaa aggatcttca cctagatcct tttaaattaa 2160

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tgcttaatca gtgaggcacc tatctcagcg atctgtctat ttcgttcatc catagctgcc 2280

tgactccccg tcgtgtagat aactacgata cgggagggct taccatctgg ccccagtgct 2340

gcaatgatac cgcgagaccc acgctcaccg gctccagatt tatcagcaat aaaccagcca 2400

gccggaaggg ccgagcgcag aagtggtcct gcaactttat ccgcctccat ccagtctatt 2460

aattgttgcc gggaagctag agtaagtagt tcgccagtta atagtttgcg caacgttgtt 2520

gccattgcta caggcatcgt ggtgtcacgc tcgtcgtttg gtatggcttc attcagctcc 2580

ggttcccaac gatcaaggcg agttacatga tcccccatgt tgtgcaaaaa agcggttagc 2640

tccttcggtc ctccgatcgt tgtcagaagt aagttggccg cagtgttatc actcatggtt 2700

atggcagcac tgcataattc tcttactgtc atgccatccg taagatgctt ttctgtgact 2760

ggtgagtact caaccaagtc attctgagaa tagtgtatgc ggcgaccgag ttgctcttgc 2820

ccggcgtcaa tacgggataa taccgcgcca catagcagaa ctttaaaagt gctcatcatt 2880

ggaaaacgtt cttcggggcg aaaactctca aggatcttac cgctgttgag atccagttcg 2940

atgtaaccca ctcgtgcacc caactgatct tcagcatctt ttactttcac cagcgtttct 3000

gggtgagcaa aaacaggaag gcaaaatgcc gcaaaaaagg gaataagggc gacacggaaa 3060

tgttgaatac tcatactctt cctttttcaa tattattgaa gcatttatca gggttattgt 3120

ctcatgagcg gatacatatt tgaatgtatt tagaaaaata aacaaatagg ggttccgcgc 3180

acatttcccc gaaaagtgcc acctgacgtc taagaaacca ttattatcat gacattaacc 3240

tataaaaata ggcgtatcac gaggcccttt cgtcttcacc tcgagaaatc ataaaaaatt 3300

tatttgcttt gtgagcggat aacaattata atagattcaa ttgtgagcgg ataacaattt 3360

cacacagaat tcattaaaga ggagaaatta accatgagtg acattgcctt cttgattgat 3420

ggctctggta gcatcatccc acatgacttt cggcggatga aggagtttgt ctcaactgtg 3480

atggagcaat taaaaaagtc caaaaccttg ttctctttga tgcagtactc tgaagaattc 3540

cggattcact ttaccttcaa agagttccag aacaacccta acccaagatc actggtgaag 3600

ccaataacgc agctgcttgg gcggacacac acggccacgg gcatccgcaa agtggtacga 3660

gagctgttta acatcaccaa cggagcccga aagaatgcct ttaagatcct agttgtcatc 3720

acggatggag aaaagtttgg cgatcccttg ggatatgagg atgtcatccc tgaggcagac 3780

agagagggag tcattcgcta cgtcattggg gtgggagatg ccttccgcag tgagaaatcc 3840

cgccaagagc ttaataccat cgcatccaag ccgcctcgtg atcacgtgtt ccaggtgaat 3900

aactttgagg ctctgaagac cattcagaac cagcttcggg agaagatctt tgcgatcgag 3960

ggtactcaga caggaagtag cagctccttt gagcatgaga tgtctcagga aatcgaaggt 4020

agacatcacc atcaccatca ctaga 4045

<210> 38

<211> 1574

<212> DNA

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: expression cassette

<400> 38
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aaaagcggct tcctgacagg aggccgtttt gttttgcagc ccacctcaac gcaattaatg 120

tgagttagct cactcattag gcaccccagg ctttacactt tatgcttccg gctcgtatgt 180

tgtgtggaat tgtgagcgga taacaatttc acacaggaaa cagctatgac catgattacg 240

aatttctaga taacgagggc aaaaaatgaa aaagacagct atcgcgattg cagtggcact 300

ggctggtttc gctaccgtag cgcaggccga ctactgcgat atcgaattcg cagaaacagt 360

tgaaagttgt ttagcaaaac cccatacaga aaattcattt actaacgtct ggaaagacga 420

caaaacttta gatcgttacg ctaactatga gggctgtctg tggaatgcta caggcgttgt 480

agtttgtact ggtgacgaaa ctcagtgtta cggtacatgg gttcctattg ggcttgctat 540

ccctgaaaat gagggtggtg gctctgaggg tggcggttct gagggtggcg gctctgaggg 600

tggcggtact aaacctcctg agtacggtga tacacctatt ccgggctata cttatatcaa 660

ccctctcgac ggcacttatc cgcctggtac tgagcaaaac cccgctaatc ctaatccttc 720

tcttgaggag tctcagcctc ttaatacttt catgtttcag aataataggt tccgaaatag 780

gcaggggca ttaactgttt atacgggcac tgttactcaa ggcactgacc ccgttaaaac 840

ttattaccag tacactcctg tatcatcaaa agccatgtat gacgcttact ggaacggtaa 900

attcagagac tgcgctttcc attctggctt taatgaggat ccattcgttt gtgaatatca 960

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ttctggtggc ggctctgagg gtggcggctc tgagggtggc ggttctgagg gtggcggctc 1080

tgagggtggc ggttccggtg gcggctccgg ttccggtgat tttgattatg aaaaaatggc 1140

aaacgctaat aaggggggcta tgaccgaaaa tgccgatgaa aacgcgctac agtctgacgc 1200

taaaggcaaa cttgattctg tcgctactga ttacggtgct gctatcgatg gtttcattgg 1260

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ccaaatggct caagtcggtg acggtgataa ttcaccttta atgaataatt tccgtcaata 1380

tttaccttct ttgcctcagt cggttgaatg tcgcccttat gtctttggcg ctggtaaacc 1440

atatgaattt tctattgatt gtgacaaaat aaacttattc cgtggtgtct ttgcgtttct 1500

tttatatgtt gccaccttta tgtatgtatt ttcgacgttt gctaacatac tgcgtaataa 1560

ggagtcttaa gctt 1574

<210> 39

<211> 932

<212> DNA

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: expression cassette

<400> 39
gctagcctga ggccagtttg ctcaggctct ccccgtggag gtaataattg ctcgaccgat 60

aaaagcggct tcctgacagg aggccgtttt gttttgcagc ccacctcaac gcaattaatg 120

tgagttagct cactcattag gcaccccagg ctttacactt tatgcttccg gctcgtatgt 180

tgtgtggaat tgtgagcgga taacaatttc acacaggaaa cagctatgac catgattacg 240

aatttctaga taacgagggc aaaaaatgaa aaagacagct atcgcgattg cagtggcact 300

ggctggtttc gctaccgtag cgcaggccga ctactgcgat atcgaattca atgctggcgg 360

cggctctggt ggtggttctg gtggcggctc tgagggtggt ggctctgagg gtggcggttc 420

tgagggtggc ggctctgagg gaggcggttc cggtggtggc tctggttccg gtgattttga 480

ttatgaaaag atggcaaacg ctaataaggg ggctatgacc gaaaatgccg atgaaaacgc 540

gctacagtct gacgctaaag gcaaacttga ttctgtcgct actgattacg gtgctgctat 600

cgatggtttc attggtgacg tttccggcct tgctaatggt aatggtgcta ctggtgattt 660

tgctggctct aattcccaaa tggctcaagt cggtgacggt gataattcac ctttaatgaa 720

taatttccgt caatatttac cttccctccc tcaatcggtt gaatgtcgcc cttttgtctt 780

tggcgctggt aaaccatatg aattttctat tgattgtgac aaaataaact tattccgtgg 840

tgtctttgcg tttcttttat atgttgccac ctttatgtat gtattttcta cgtttgctaa 900

catactgcgt aataaggagt cttgataagc tt 932

<210> 40

<211> 4425

<212> DNA

<213> artificial sequence

<220>
<223> Description of Artificial Sequence: vector

<400> 40
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ggtttcgcta ccgtagcgca ggccgactac tgcgatatcg aattcgcaga aacagttgaa 120

agttgtttag caaaacccca tacagaaaat tcatttacta acgtctggaa agacgacaaa 180

actttagatc gttacgctaa ctatgagggc tgtctgtgga atgctacagg cgttgtagtt 240

tgtactggtg acgaaactca gtgttacggt acatgggttc ctattgggct tgctatccct 300

gaaaatgagg gtggtggctc tgagggtggc ggttctgagg gtggcggctc tgagggtggc 360

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ctcgacggca cttatccgcc tggtactgag caaaaccccg ctaatcctaa tccttctctt 480

gaggagtctc agcctcttaa tactttcatg tttcagaata ataggttccg aaataggcag 540

ggggcattaa ctgtttatac gggcactgtt actcaaggca ctgaccccgt taaaacttat 600

taccagtaca ctcctgtatc atcaaaagcc atgtatgacg cttactggaa cggtaaattc 660

agagactgcg ctttccattc tggctttaat gaggatccat tcgtttgtga atatcaaggc 720

caatcgtctg acctgcctca acctcctgtc aatgctggcg gcggctctgg tggtggttct 780

ggtggcggct ctgagggtgg cggctctgag ggtggcggtt ctgagggtgg cggctctgag 840

ggtggcggtt ccggtggcgg ctccggttcc ggtgattttg attatgaaaa aatggcaaac 900

gctaataagg gggctatgac cgaaaatgcc gatgaaaacg cgctacagtc tgacgctaaa 960

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cgtgaaaggc cgttttacca tttcacgtga taattcgaaa aacaccctgt atctgcaaat 1680

gaacagcctg cgtgcggaag atacggccgt gtattattgc gcgcgtcgtt ctggtgctta 1740

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tacgaaagtt gaaattaaac gtacggaatt cccaggggggg agcggaggcg cgccgcacca 2220

tcatcaccat cactgctgat aagcttgacc tgtgaagtga aaaatggcgc agattgtgcg 2280

acatttttt tgtctgccgt ttaatgaaat tgtaaacgtt aatattttgt taaaattcgc 2340

gttaaatttt tgttaaatca gctcattttt taaccaatag gccgaaatcg gcaaaatccc 2400

ttataaatca aaagaataga ccgagatagg gttgagtgtt gttccagttt ggaacaagag 2460

tccactatta aagaacgtgg actccaacgt caaagggcga aaaaccgtct atcagggcga 2520

tggcccacta cgagaaccat caccctaatc aagtttttg gggtcgaggt gccgtaaagc 2580

actaaatcgg aaccctaaag ggagcccccg atttagagct tgacggggaa agccggcgaa 2640

cgtggcgaga aaggaaggga agaaagcgaa aggagcgggc gctagggcgc tggcaagtgt 2700

agcggtcacg ctgcgcgtaa ccaccacacc cgccgcgctt aatgcgccgc tacagggcgc 2760

gtgctagcca tgtgagcaaa aggccagcaa aaggccagga accgtaaaaa ggccgcgttg 2820

ctggcgtttt tccataggct ccgccccccct gacgagcatc acaaaaatcg acgctcaagt 2880

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